

Vollenhovia emeryi QTL mapping

```
library(qtl)
```

```
## Loading required package: parallel
```

```
library(ggplot2)
```

```
# read phenotypes and map  
cross <- read.cross("csv",  
  "/Users/sasha/Dropbox/projects/vollenhovia/", "map.csv",  
  estimate.map = FALSE)
```

```
## --Read the following data:  
## 222 individuals  
## 1956 markers  
## 3 phenotypes
```

```
## Warning: Some markers at the same position on chr  
## 1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18; use jittermap().
```

```
## --Cross type: bc
```

```
error_rate <- 0.00126 #estimated from GQ data  
cross <- jittermap(cross)  
  
# plotMap(cross, show.marker.names=FALSE)  
  
cross <- calc.genoprob(cross, error.prob = error_rate, map.function  
= "haldane")  
summary(cross)
```

```
##      Backcross
##
##      No. individuals:      222
##
##      No. phenotypes:      3
##      Percent phenotyped: 100 100 29.7
##
##      No. chromosomes:     18
##      Autosomes:           1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16
17 18
##
##      Total markers:       1956
##      No. markers:         186 179 171 167 161 113 119 114 89 92 85
85 79 72
##
##      Percent genotyped:    75 60 62 47
##      Genotypes (%):       AA:48.8  AB:51.2
```

```
sex_scan <- scanone(cross, pheno.col = 2, model = "binary", method
= "em")
```

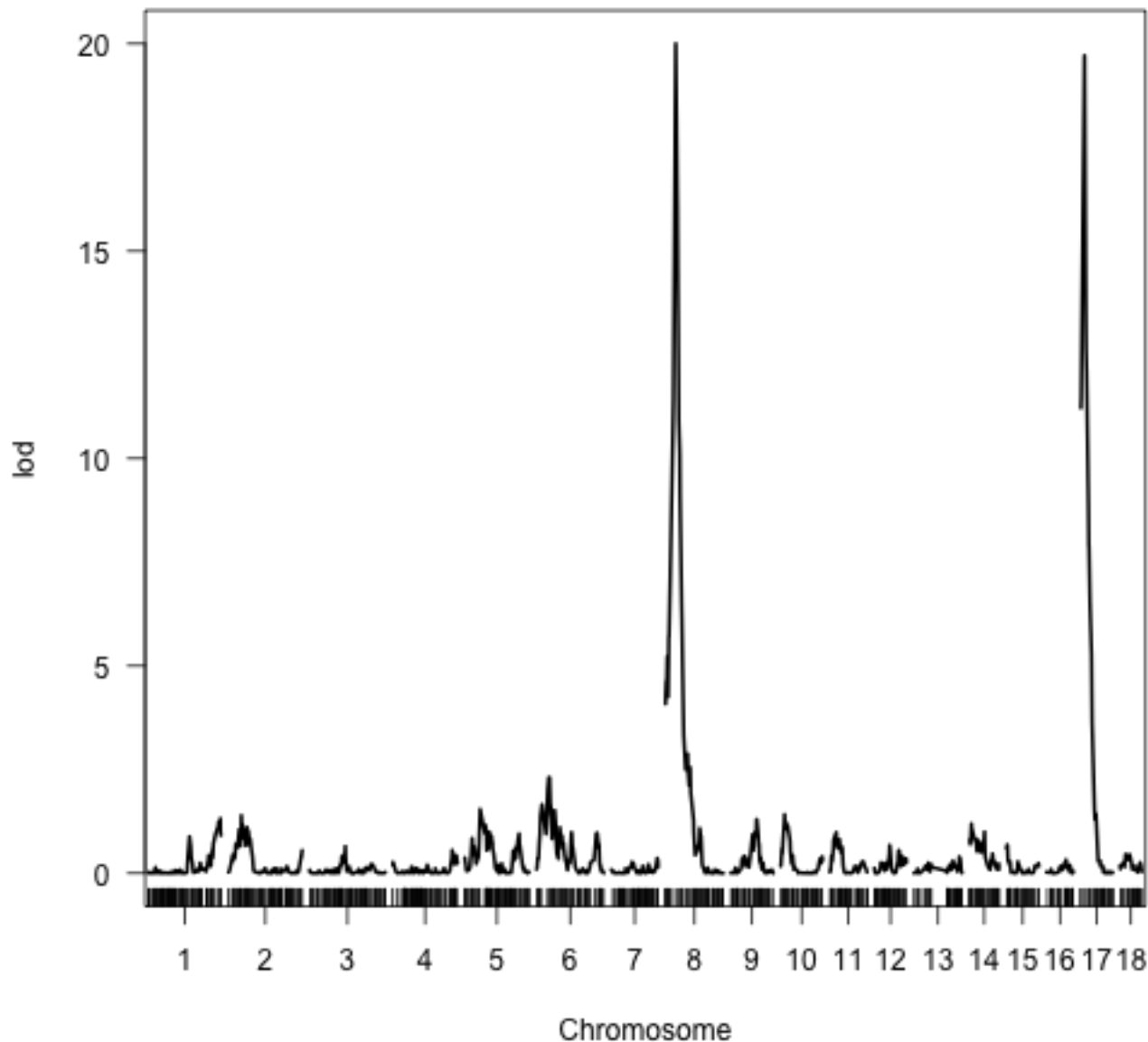
```
sex_scan_perm <- scanone(cross, pheno.col = 2, model = "binary",
method = "em",
n.perm = 1000)
```

```
## Permutation 20
## Permutation 40
## Permutation 60
## Permutation 80
## Permutation 100
## Permutation 120
## Permutation 140
## Permutation 160
## Permutation 180
## Permutation 200
## Permutation 220
## Permutation 240
## Permutation 260
## Permutation 280
## Permutation 300
## Permutation 320
## Permutation 340
## Permutation 360
## Permutation 380
## Permutation 400
## Permutation 420
## Permutation 440
## Permutation 460
## Permutation 480
## Permutation 500
## Permutation 520
## Permutation 540
## Permutation 560
## Permutation 580
## Permutation 600
## Permutation 620
## Permutation 640
## Permutation 660
## Permutation 680
## Permutation 700
## Permutation 720
## Permutation 740
## Permutation 760
## Permutation 780
## Permutation 800
## Permutation 820
## Permutation 840
## Permutation 860
## Permutation 880
## Permutation 900
## Permutation 920
## Permutation 940
## Permutation 960
## Permutation 980
## Permutation 1000
```

```
summary(sex_scan, perms = sex_scan_perm, alpha = 0.05, pvalues =
TRUE)
```

```
##          chr  pos  lod  pval
## contig07369_3776    8 34.1 20.0    0
## contig03622_6037   17 12.2 19.7    0
```

```
plot(sex_scan)
```



```
cp <- as.numeric(summary(sex_scan, perms = sex_scan_perm, alpha =
0.05, pvalues = TRUE)$chr)
qp <- summary(sex_scan, perms = sex_scan_perm, alpha = 0.05,
pvalues = TRUE)$pos

cross <- sim.geno(cross)
qtl <- makeqtl(cross, cp, qp)

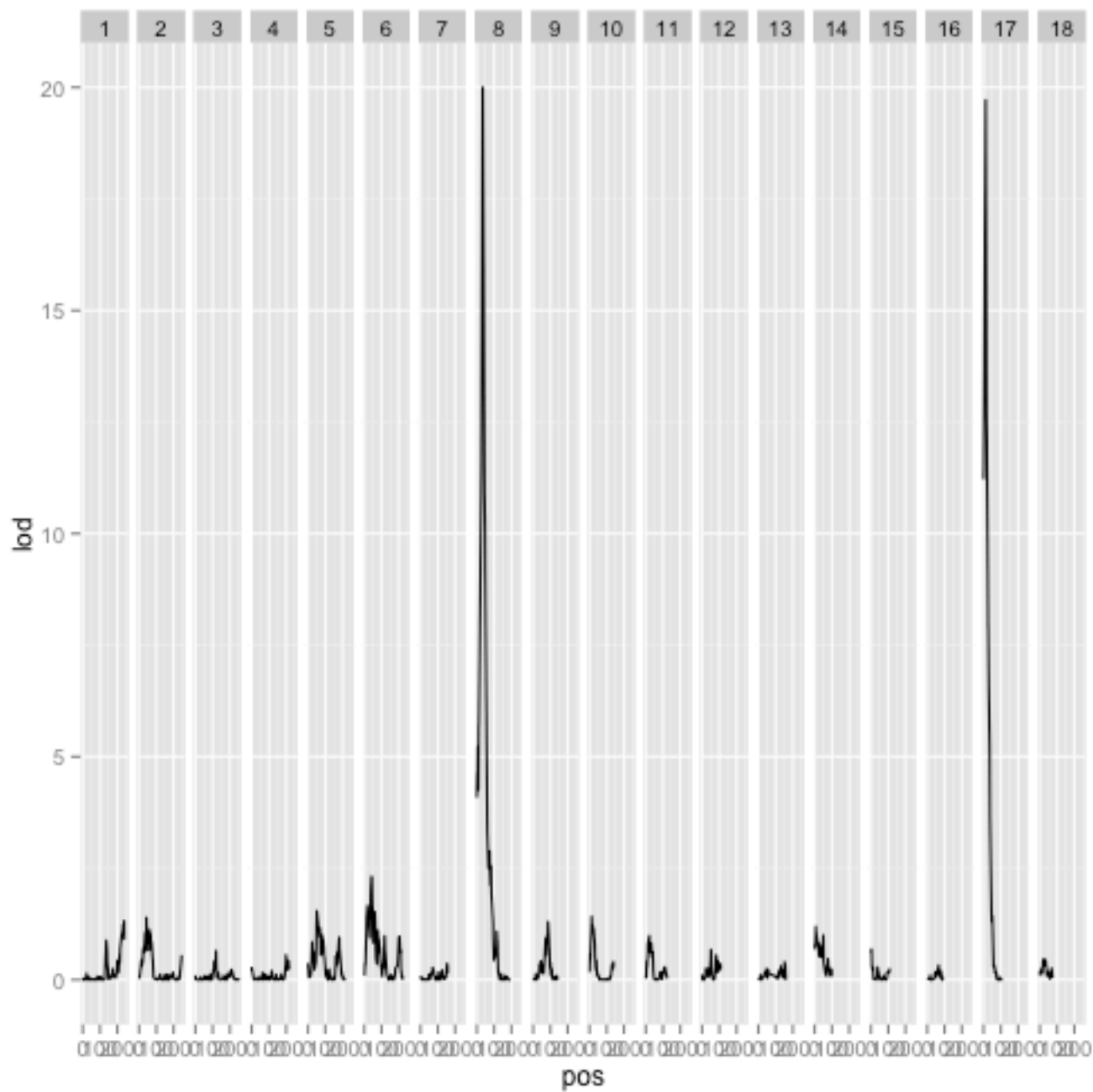
lod.sex <- fitqtl(cross, pheno.col = 2, qtl, formula = y ~ Q1 * Q2,
method = "hk")
```

```
## warning: The qtl object doesn't contain QTL genotype
probabilities; using
## method="imp".
```

summary(lod.sex)

```
##
##      fitqtl summary
##
## Method: multiple imputation
## Model:  normal phenotype
## Number of observations : 222
##
## Full model result
## -----
## Model formula: y ~ Q1 + Q2 + Q1:Q2
##
##      df      SS      MS    LOD  %var Pvalue(Chi2) Pvalue(F)
## Model    3 41.531 13.84365 108.9 89.55           0           0
## Error 218  4.847  0.02224
## Total 221 46.378
##
##
## Drop one QTL at a time ANOVA table:
## -----
##      df Type III SS    LOD  %var F value Pvalue(Chi2)
## Pvalue(F)
## 8@34.1      2      25.80 88.91 55.64   580.2           0
## <2e-16
## 17@12.2     2      26.23 89.56 56.55   589.7           0
## <2e-16
## 8@34.1:17@12.2 1      11.47 58.50 24.72   515.6           0
## <2e-16
##
## 8@34.1      ***
## 17@12.2     ***
## 8@34.1:17@12.2 ***
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
ggplot(sex_scan, aes(x = pos, y = lod, group = chr)) + geom_line()
+ facet_grid(~chr)
```



```
# for(i in cp) print(bayesint(sex_scan,chr=i,prob=0.99))
for (i in cp) print(lodint(sex_scan, chr = i))
```

```
##          chr    pos    lod
## contig04905_5563    8 26.19 11.41
## contig07369_3776    8 34.13 20.00
## contig02399_617     8 38.88 16.40
##          chr    pos    lod
## contig09451_4024   17  1.022 11.46
## contig03622_6037   17 12.176 19.71
## contig04281_5059   17 17.353 12.65
```